We claim:

1. A method for producing ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites by culturing organisms which have

a reduced Δ22-desaturase activity and

an increased HMG-CoA-reductase activity and

an increased activity of at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity

in comparison with the wild type.

2. A method as claimed in claim 1, wherein, in order to reduce the Δ22-desaturase activity, the gene expression of a nucleic acid encoding a Δ22-desaturase is reduced in comparison with the wild type.

3. A method as claimed in claim 2, wherein an organism without a functional Δ22-desaturase gene is used.

4. A method as claimed in any of claims 1 to 3, wherein, in order to increase the HMG-CoA reductase activity, the gene expression of a nucleic acid encoding an HMG-CoA reductase is increased in comparison with the wild type.

5. A method as claimed in claim 4, wherein, in order to increase gene expression, a nucleic acid construct comprising a nucleic acid encoding an HMG-CoA reductase is introduced into the organism and whose expression in the organism is subject to reduced regulation in comparison with the wild type.

6. A method as claimed in claim 5, wherein the nucleic acid construct comprises a promoter which, in the organism, is subject to reduced regulation in comparison with the wild-type promoter.

7. A method as claimed in claim 6, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid whose expression in the organism is subject to reduced regulation in comparison with the homologous, orthologous nucleic acid.

8. A method as claimed in claim 7, wherein the nucleic acid encoding an HMG-CoA reductase is a nucleic acid which encodes the catalytic region of HMG-CoA reductase.

9. A method as claimed in claim 8, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 4 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 4 at the amino acid level which, proteins have the enzymatic characteristic of an HMG-CoA reductase.

10. A method as claimed in claim 9, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 3 is introduced.

11. A method as claimed in any of claims 1 to 10, wherein, in order to increase the lanosterol C14-demethylase activity, the gene expression of a nucleic acid encoding a lanosterol C14-demethylase is increased in comparison with the wild type.

12. A method as claimed in claim 11, wherein, in order to increase gene expression, one or more nucleic acids encoding a lanosterol C14-demethylase are introduced into the organism.

13. A method as claimed in claim 12, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 6 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 6 at the amino acid level, which proteins have the enzymatic characteristic of a lanosterol C14-demethylase.

14. A method as claimed in claim 13, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 5 is introduced.

15. A method as claimed in any of claims 1 to 14, wherein, in order to increase the squalene epoxidase activity, the gene expression of a nucleic acid encoding a squalene epoxidase is increased in comparison with the wild type.

16. A method as claimed in claim 15, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene epoxidase are introduced into the organism.

17. A method as claimed in claim 16, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 8 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 8 at the amino acid level, which proteins have the enzymatic characteristic of a squalene epoxidase.

18. A method as claimed in claim 17, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 7 is introduced.

19. A method as claimed in any of claims 1 to 18, wherein, in order to increase the squalene synthetase activity, the gene expression of a nucleic acid encoding a squalene synthetase is increased in comparison with the wild type.

20. A method as claimed in claim 19, wherein, in order to increase gene expression, one or more nucleic acids encoding a squalene synthetase are introduced into the organism.

21. A method as claimed in claim 20, wherein the nucleic acids introduced are nucleic acids encoding proteins comprising the amino acid sequence SEQ. ID. NO. 10 or a sequence derived from this sequence by substitution, insertion or deletion of amino acids which has at least 30% identity with the sequence SEQ. ID. NO. 10 at the amino acid level, which proteins have the enzymatic characteristic of a squalene synthetase.

22. A method as claimed in claim 21, wherein a nucleic acid comprising the sequence SEQ. ID. NO. 9 is introduced.

23. A method as claimed in any of claims 1 to 22, wherein the organism used is yeast.

24. A method as claimed in any of claims 1 to 23, wherein, after the cultivation, the organism is harvested and ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites are subsequently isolated from the organism.

25. A genetically modified organism, where the genetic modification

reduces the Δ22-desaturase activity and

increases the HMG-CoA reductase activity and

increases at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity

in comparison with the wild type.

26. A genetically modified organism as claimed in claim 25, where the genetic modification

reduces the Δ22-desaturase activity and

increases the HMG-CoA reductase activity and

increases the lanosterol C14-demethylase activity

in comparison with the wild type.

27. A genetically modified organism as claimed in claim 25 or 26, wherein the genetically modified organism has an increased content in ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites in comparison with the wild type.

28. A genetically modified organism as claimed in claim 25 or 26, wherein the organism used is yeast.

29. The use of a genetically modified organism as claimed in any of claims 25 to 27 for the production of ergosta-5,7-dienol and/or its biosynthetic intermediates and/or metabolites.

30. A method for the generation of a genetically modified organism in which, starting from a starting organism,

the Δ22-desaturase activity is reduced and

the HMG-CoA reductase activity is increased and

at least one of the activities selected from the group consisting of lanosterol C14-demethylase activity, squalene epoxidase activity and squalene synthetase activity is increased.